

SEQUENCE LISTING

<110> Degussa AG

<120> A process for producing L-amino acids using strains of the Enterobacteriaceae family

<130> 020481 BT

<160> 4

<170> PatentIn version 3.1

<210> 1

<211> 32

<212> DNA

<213> Synthetic sequence

<220>

<221> Primer

<222> (1)..(32)

<223> galP1

<400> 1

cacaatctag ataaaccata ttggagggca tc

32

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<211> 25

<212> DNA

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<222> (1)..(25)

<223> galP2

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gggaggaagc ttggggagat taatc

25

<210> 3

<211> 1446

<212> DNA

<213> Escherichia coli

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<221> DNA fragment

<222> (1)..(1446)

<223> PCR product

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<221> CDS

<222> (33)..(1427)
<223> galP coding region

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ttg cag gtt aaa cag agt ggc tgg gcg ctg ttt aaa gag aac agc aac Leu Gln Val Lys Gln Ser Gly Trp Ala Leu Phe Lys Glu Asn Ser Asn 235 240 245	773
ttc cgc cgc gcg gtg ttc ctt ggc gta ctg ttg cag gta atg cag caa Phe Arg Arg Ala Val Phe Leu Gly Val Leu Leu Gln Val Met Gln Gln 250 255 260	821
ttc acc ggg atg aac gtc atc atg tat tac gcg ccg aaa atc ttc gaa Phe Thr Gly Met Asn Val Ile Met Tyr Tyr Ala Pro Lys Ile Phe Glu 265 270 275	869
ctg gcg ggt tat acc aac act acc gag caa atg tgg ggg acc gtg att Leu Ala Gly Tyr Thr Asn Thr Glu Gln Met Trp Gly Thr Val Ile 280 285 290 295	917
gtc ggc ctg acc aac gta ctt gcc acc ttt atc gca atc ggc ctt gtt Val Gly Leu Thr Asn Val Leu Ala Thr Phe Ile Ala Ile Gly Leu Val 300 305 310	965
gac cgc tgg gga cgt aaa cca acg cta acg ctg ggc ttc ctg gtg atg Asp Arg Trp Gly Arg Lys Pro Thr Leu Thr Leu Gly Phe Leu Val Met 315 320 325	1013
gct gct ggc atg ggc gta ctc ggt aca atg atg cat atc ggt att cac Ala Ala Gly Met Gly Val Leu Gly Thr Met Met His Ile Gly Ile His 330 335 340	1061
tct ccg tcg gcg cag tat ttc gcc atc gcc atg ctg ctg atg ttt att Ser Pro Ser Ala Gln Tyr Phe Ala Ile Ala Met Leu Leu Met Phe Ile 345 350 355	1109
gtc ggt ttt gcc atg agt gcc ggt ccg ctg att tgg gta ctg tgc tcc Val Gly Phe Ala Met Ser Ala Gly Pro Leu Ile Trp Val Leu Cys Ser 360 365 370 375	1157
gaa att cag ccg ctg aaa ggc cgc gat ttt ggc atc acc tgc tcc act Glu Ile Gln Pro Leu Lys Gly Arg Asp Phe Gly Ile Thr Cys Ser Thr 380 385 390	1205
gcc acc aac tgg att gcc aac atg atc gtt ggc gca acg ttc ctg acc Ala Thr Asn Trp Ile Ala Asn Met Ile Val Gly Ala Thr Phe Leu Thr 395 400 405	1253
atg ctc aac acg ctg ggt aac gcc aac acc ttc tgg gtg tat gcg gct Met Leu Asn Thr Leu Gly Asn Ala Asn Thr Phe Trp Val Tyr Ala Ala 410 415 420	1301
ctg aac gta ctg ttt atc ctg ctg aca ttg tgg ctg gta ccg gaa acc Leu Asn Val Leu Phe Ile Leu Leu Thr Leu Trp Leu Val Pro Glu Thr 425 430 435	1349
aaa cac gtt tcg ctg gaa cat att gaa cgt aat ctg atg aaa ggt cgt Lys His Val Ser Leu Glu His Ile Glu Arg Asn Leu Met Lys Gly Arg 440 445 450 455	1397
aaa ctg cgc gaa ata ggc gct cac gat taa tctccccaaag cttccccc Lys Leu Arg Glu Ile Gly Ala His Asp 460	1446

<210> 4

<211> 464

<212> PRT

<213> Escherichia coli

<400> 4

Met Pro Asp Ala Lys Lys Gln Gly Arg Ser Asn Lys Ala Met Thr Phe
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Phe Val Cys Phe Leu Ala Ala Leu Ala Gly Leu Leu Phe Gly Leu Asp
20 25 30

Ile Gly Val Ile Ala Gly Ala Leu Pro Phe Ile Ala Asp Glu Phe Gln
35 40 45

Ile Thr Ser His Thr Gln Glu Trp Val Val Ser Ser Met Met Phe Gly
50 55 60

Ala Ala Val Gly Ala Val Gly Ser Gly Trp Leu Ser Phe Lys Leu Gly
65 70 75 80

Arg Lys Lys Ser Leu Met Ile Gly Ala Ile Leu Phe Val Ala Gly Ser
85 90 95

Leu Phe Ser Ala Ala Ala Pro Asn Val Glu Val Leu Ile Leu Ser Arg
100 105 110

Val Leu Leu Gly Leu Ala Val Gly Val Ala Ser Tyr Thr Ala Pro Leu
115 120 125

Tyr Leu Ser Glu Ile Ala Pro Glu Lys Ile Arg Gly Ser Met Ile Ser
130 135 140

Met Tyr Gln Leu Met Ile Thr Ile Gly Ile Leu Gly Ala Tyr Leu Ser
145 150 155 160

Asp Thr Ala Phe Ser Tyr Thr Gly Ala Trp Arg Trp Met Leu Gly Val
165 170 175

Ile Ile Ile Pro Ala Ile Leu Leu Ile Gly Val Phe Phe Leu Pro
180 185 190

Asp Ser Pro Arg Trp Phe Ala Ala Lys Arg Arg Phe Val Asp Ala Glu
195 200 205

Arg Val Leu Leu Arg Leu Arg Asp Thr Ser Ala Glu Ala Lys Arg Glu
210 215 220

Leu Asp Glu Ile Arg Glu Ser Leu Gln Val Lys Gln Ser Gly Trp Ala
225 230 235 240

Leu Phe Lys Glu Asn Ser Asn Phe Arg Arg Ala Val Phe Leu Gly Val
245 250 255

Leu Leu Gln Val Met Gln Gln Phe Thr Gly Met Asn Val Ile Met Tyr
260 265 270

Tyr Ala Pro Lys Ile Phe Glu Leu Ala Gly Tyr Thr Asn Thr Thr Glu
275 280 285

Gln Met Trp Gly Thr Val Ile Val Gly Leu Thr Asn Val Leu Ala Thr
290 295 300

Phe Ile Ala Ile Gly Leu Val Asp Arg Trp Gly Arg Lys Pro Thr Leu
305 310 315 320

Thr Leu Gly Phe Leu Val Met Ala Ala Gly Met Gly Val Leu Gly Thr
325 330 335

Met Met His Ile Gly Ile His Ser Pro Ser Ala Gln Tyr Phe Ala Ile
340 345 350

Ala Met Leu Leu Met Phe Ile Val Gly Phe Ala Met Ser Ala Gly Pro
355 360 365

Leu Ile Trp Val Leu Cys Ser Glu Ile Gln Pro Leu Lys Gly Arg Asp
370 375 380

Phe Gly Ile Thr Cys Ser Thr Ala Thr Asn Trp Ile Ala Asn Met Ile
385 390 395 400

Val Gly Ala Thr Phe Leu Thr Met Leu Asn Thr Leu Gly Asn Ala Asn
405 410 415

Thr Phe Trp Val Tyr Ala Ala Leu Asn Val Leu Phe Ile Leu Leu Thr
420 425 430

Leu Trp Leu Val Pro Glu Thr Lys His Val Ser Leu Glu His Ile Glu
435 440 445

Arg Asn Leu Met Lys Gly Arg Lys Leu Arg Glu Ile Gly Ala His Asp
450 455 460